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NOTES

Standardized and Simplified Nomenclature for Proteins Common to All Retroviruses

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We propose a revised standardized nomenclature for the proteins common to all retroviruses on the basis of biological function, enzymatic activity, and/or virion location data. (We do not discuss proteins specific for subfamilies or only some retroviruses.)

During the past decade, the retrovirus proteins have been designated by the letter "p" followed by an approximate molecular weight estimated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis or gel filtration data (1). original molecular weight estimates for some of the proteins were inaccurate.

We propose a unified nomenclature for retrovirus proteins on the basis of known biological function, location in virions,

TABLE 1. Proposed nomenclature for proteins common to all retroviruses

Virus	Name of protein[a]								
	MA	?[b]	CA	NC	PR	RT	IN	SU	TM
ASLV	p19	p10	p27	p12	p15	p68	p32	gp85	gp37
MuLV	p15	p12	p30	p10	p14	p80	p46	gp70	p15E
Mouse mammary tumor virus	p10	p21	p27	p14	p13	—[c]	—	gp52	gp36
Mason-Pfizer monkey virus[d]	p10	p18	p27	p14	—	—	—	gp70	gp22
Bovine leukemia virus	p15		p24	p12	p14	—	—	gp60	gp30
Human T-cell leukemia virus type I	p19		p24	p15	p14	—	—	gp46	gp21
Equine infectious anemia virus[e]	p15		p26	p11	—	—	—	gp90	gp45
Human immunodeficiency virus type I	p17		p25	p7	p12	p66	p32	gp120	gp41

[a] Order of proteins is 5′ to 3′ on the viral genome, from left to right.
[b] ?, The nomenclature is not being changed at this time since protein function has not been elucidated.
[c] —, Size of the protein has not yet been determined.
[d] Description of proteins found in Henderson et al. (2) and Sonigo et al. (5).
[e] Description of proteins found in Stephens et al. (6), Rushlow et al., (4), and Henderson et al. (3).

As more information concerning the general properties of these proteins has accumulated, this nomenclature has proven to be cumbersome. This problem is particularly evident in the discussion of proteins from different retrovirus species for which proteins of different functions have similar molecular weights or proteins of similar functions have different molecular weights. In addition, the availability of nucleotide and protein sequence data has shown that the and/or enzymatic activity. The nomenclature will use only two letters composed of either the first two letters of a single word or the first letters of a double-word description of the protein. The two-letter notation is preferred over a three-letter notation to distinguish the protein names from those used for genes, i.e., *gag*, *pol*, and *env*. Examples of the proposed nomenclature for several retroviruses are in Table 1.

The acronyms chosen are: MA, matrix protein; CA, capsid protein; NC, nucleocapsid protein; PR, protease; RT,

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reverse transcriptase; IN, integration protein; SU, surface protein; and TM, transmembrane protein. A review of the biochemical and biological properties of the proteins from which the assignments have been made can be found in Weiss et al. (7). An example of the use of the new acronyms follows. The avian sarcoma and leukosis virus (ASLV) p15 protease would be referred to as the ASLV PR, or the murine leukemia virus (MuLV) p10 nucleocapsid protein would be referred to as the MuLV NC. In cases in which it is important to indicate the gene origin of a protein, the use of a superscript is recommended (e.g., PR^{gag}).

An acronym has not been chosen for the ASLV p10, MuLV p12, mouse mammary tumor virus p21, or Mason-Pfizer monkey virus p18 because information about their virion locations or functions is lacking. It is recommended that the old nomenclature be used in these cases.

We believe that this system is appropriate to use at this time because it is based on our increased understanding of viral functions. Additional advantages are (i) it is simple, (ii) it avoids confusion in describing the proteins of similar function in different virus species, and (iii) it is similar to nomenclature used for other animal viruses.

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